

1 GCTGTGGAA CCTCTCCAG CGCAGCAACT CAGCCAAACGA TTTCTGATAG ATTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC
CGACACCCCTT GGAGAGGTGC GCGTGTCTGA GTCGGTTGCT AAAGACTATC TAAAAACCCCT CAAACTGGTC TCTACGTTC CCACCTTCCTC GCGAAGGAG

101 CGTTAGGAA CTCTGGGAC AGAGGGCCC GCGCGCTGA TGGCCGAGG AGGGTGGAC CCAGGACCCA GGACGGCGTC GGAACCCATA CCATGGCCCG
GCAATCCCTT GAGACCCCTG TCTCGCGGG CCGCGGACT ACCGGCTCCG TCCCACGCTG GGTCTGGGT CCTTGGTAT GGTACCGGCGC
MetalArg

201 GATCCCCAAG ACCCTAAAGT TCGTCTGCTG CATCTGCTGG GTCCTGCTGC CAGTCTTAGC TTAATCTGCC ACCACTGCCC GGCAGGAGGA AGTTCCCCAG
CTAGGGGTTT TGGGATTTC AGCAGCAGCA GTAGCAGCG CAGGACGAC GTGAGGATCG AATGAGACGG TGGTGACGG CCGTCTCCT TCAAGGGGTC

4 IleProLys ThrLeuLys heValValva lIleValala ValLeuLeuP roValLeuAl aTyrSerAla ThrThrAlaA rgGlnGluGlu uValProGln

301 CAGACAGTGG CCCACAGCA ACAGAGGCAC AGCTTCAAG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCGTGCA
GTCTGTACC GGGGTGCTG TGTCTCCGTG TCGAAGTCC CCTCTCTCAC AGGTGCTCT AGAGTATCTA GTCTGTATG ACCTCGGACA TTGGGGACGT

37 GlnThrVala laProGlnG lInArgHis SerPheLysG lyGluGluCy sproAlaGly SerHisArgS erGluHisTh rGlyAlaCys AsnProCysThr

401 CAGAGGGTGT GGATTACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTTGTAAATC AGATCAAAAA CATAAAAGTT CCTGCACCAT
GTCTCCACA CCTAATGTG TTGCGAAGGT TGTACTTGG AAGAAGGAG GGTACATGTC AAACATTTAG TCTAGTTTTT GTATTTTCAA GGACGTGTA

71 GluglyVa laspTyrThr AsnAlaSerA snAsnGluPr oSerCysPhe ProCysThrV alCysLysse rAspGlnLys HisLysSers erCysThrMet

501 GACCAGAGAC ACAGTGTGTC AGTGTAAAGA AGGCACCTTC CGGAATGAAA ACTCCCCAGA GATGTGCCGG AAGTGTAGCA GGTGCCCTAG TGGGGAAAGTC
CTGGTCTCTG TGTACACACAG TCACATTTCT TCCGTGGAAG GCCTTACTTT TGAGGGGTCT CTACACGGCC TTCACATCGT CCACGGGATC ACCCTTTCAG

104 ThrArgAsp ThrValCysG lncysLysG lUglyThrPhe ArgAsnGluA snSerProG l uMetCysArg LysCysSera rGysProse rGlyGluVal

601 CAAGTCAGTA ATTGTACGTC CTGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCCAAT GCCACTGTGG AAACCCCGAG TGCTGAAGAG ACAATGAACA
GTTGAGTCTAT TAACATGTCAG GACCCCTACTA TAGGTACAC ACCTTCTTAA ACCACGGTTA CCGTGACACC TTTGGGGTGC ACGACTTCTC TGTACTTGT

137 GlnValSera snCysThrse rTrpAspAsp lIleGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr

701 CCAGCCCGG GACTCCTGCC CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG
GGTCGGGCCC CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGTGGTGC GTCCCTGAG GACGGGGTGC ACGACTTCTC TGTACTTGT GGTGGGGCCC

171 SerProG l yThrProAla ProAlaAlaG luGluThrMe tAsnThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGly

801 GACTCCTGCC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGGACTC CTGCCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG GACTCCTGCC
CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGTGGTGC GTCCCTGAG GACGGGGTGC ACGACTTCTC TGTACTTGT GGTGGGGCCC CTGAGGACGG

204 ThrProAla ProAlaAlaG luGluThrMe tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProG l yThrProAla

901 TCTTCTCATT ACCTCTCATG CACCATCGTA GGGATCATAG TTCTAATTGT GCTTCTGATT GTTTTGTGTT GAAAGACTTC ACTGTGGAAG AAATTCCTTC
AGAAAGATAA TGGAGAGTAC GTGGTAGCAT CCTAGTATC AAGATTAA CAAGAACTAA CACAAACAAA CTTTCTGAAG TGACACCTTC TTTAAGGAAG

237 SerSerHisT yrLeuSerCy sThrIleVal GlyIleIleVal lleuLeuIle valPheVal

1001 CTTACTTGAA AGGTTAGGT AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCCTCC TCTGCTGTGT TCCACACAG AGAAACGCCT
GAATGGACTT TCCAAGTCCA TCCGGGACCG ACTCCGCCCC CCGCGGACCG GTGAGAGACG GGACGGAGG AGACGACACA AGGTGTCTG TCTTTCGGA

1101 GCCCCTGCC CAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA
CGGGACGGG GTTTTTTTT TTTTTTTT TTTTTTTT TTTTTTTT TTTTTTTT TTTTTTTT TTTTTTTT TTTTTTTT

[illegible]

Apo2	1	-----MEQRGQNAPAAAGARKRHGPGPREARGARPGLRVPKTLVL
Apo2DcR	1	-----MARIPKTLKFVV
DR4	51	GRGALPTSMGQHGPSARARAGRAPGPPAREASPRLRVHKTFFKFVVVGVL
Apo2	41	VVAAVLLLVSAESALITQODLAPQRAAPQOKESSPSEGLCPPGHHISED
Apo2DcR	13	VIVAVLLPVLAYSATTAQEEVPOQTVAPQQRHSFKGEECPAGSHRSEH
DR4	101	LQVVPSSAATIK-----LHDQSIGTQWEHSPGLGELCPPGSHRSEH
Apo2	91	GRDCISCKYGDYSTHWN [↓] DLFLCRLCTRCDSGEVELSPCTTTRNTVCOCE
Apo2DcR	63	TGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCTMTTRDTVCOCK
DR4	142	PGACNRCTEGVGYNASNNEFACLPCTACKSDEEERSPCTTTRNTACOCK
Apo2	141	EGTFREEDSP ^{CRD1} EMCRKCR ^{CRD1} TGCPRGMVKVGDC ^{CRD1} TFWSDIECVHKE-----
Apo2DcR	113	EGTFERNENSP ^{CRD2} EMCRKCSR-CPSGEVOVS ^{CRD2} NCTSWDDIOCVE-EFGANATVE
DR4	192	PGTFERNDNSAEMCRKCS ^{CRD2} TGCPRGMVKVGDC ^{CRD2} TFWSDIECVHKE-----
Apo2	161	TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAE
Apo2DcR	211	ETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV
DR4	234	-----SGNGHN ^{SGIT} IWVILVVTLVVPIILLVAV-LIVC
Apo2	203	CKSLLWKKVLPYLKGICSGGGGDPERVDRSSQRPGAEDNVLNEIVSILQP
DR4	262	CCIGSGCGGDPKCMDRVCFWRLGLLRGPGAEDNAHNEILSNADSLSTFVS
Apo2	253	TQVPEQEMEVOEPAEPTGVNMLSPGESEHLLPEAEAEERSORRRRLIVPANE
DR4	312	----EQOMESQEPADLTGVTVQSPGEAQCLLGPAEAEGSORRRRLIVPANG
Apo2	303	GDPTETLRQCFDDFADLVPPFDSWEPI [*] MRKLG [*] IMDNEIKVAKAEAAAGH--R
DR4	358	ADPTETLMLFFEDKFANIVPPFDSWDQLMRQDLTKNEIDVV [*] RAGTAGP--G
Apo3/DR3	338	VMDAVPARRWKEFVRTLGLREAEIEAVEVEI-GRF-R
TNFR1	322	VVENVPPLRWKEFVERLGLSDHEIDRIELON-GRCLR
CD95	220	IAGVHTLSQVKGFVRKNGVNEAKIDEIKNDN-VQDTA
Apo2	351	DTLYTMLIKWVNKTGR-DASVHTLLDALET [*] LG [*] ERLAKOK [*] IEDHLLSSGKF
DR4	406	DALYAMLKMWVNKTGR-NASHTLLDALERMEERHAK [*] EKIQD [*] LLVDSGKF
Apo3/DR3	374	DOQYEMLKRW [*] RQQP---AGLGAVYAALERMGLDCCVEDLRS
TNFR1	358	EAQYSMLATWRRRT [*] PPREATLELLGRVLRDM [*] DLG [*] CLEDIEE
CD95	256	EQKVQLLRNWHQLHGKKEAY-DT [*] LIK [*] DEK [*] KANLCTLA [*] EKIQT
Apo2	400	MYLEGNADSALS
DR4	455	IYLEDGTGSAVSLE

Fig. 2

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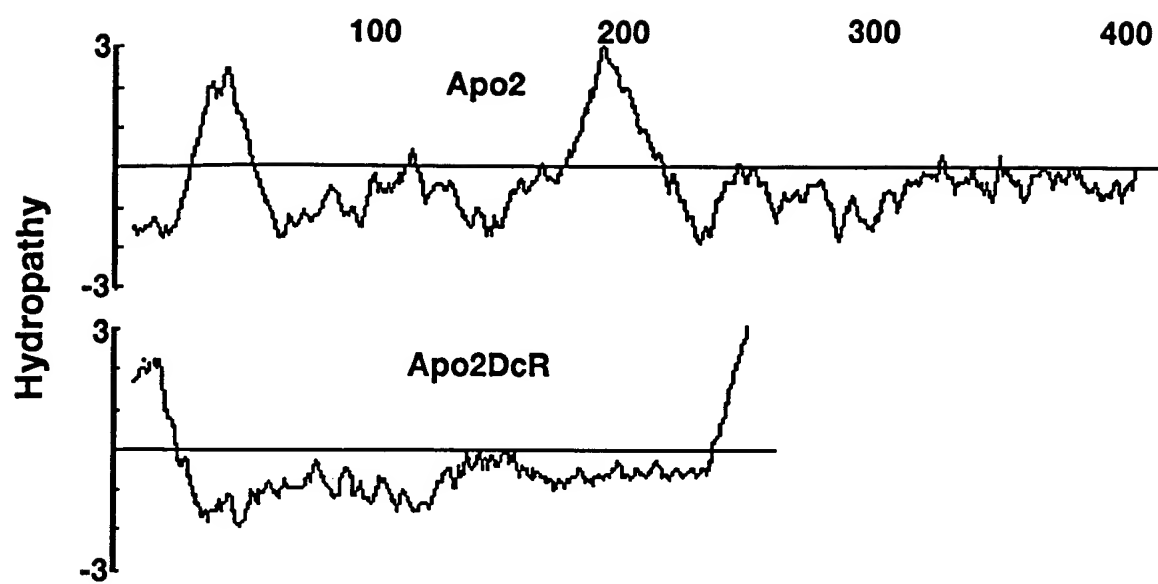


Figure 3

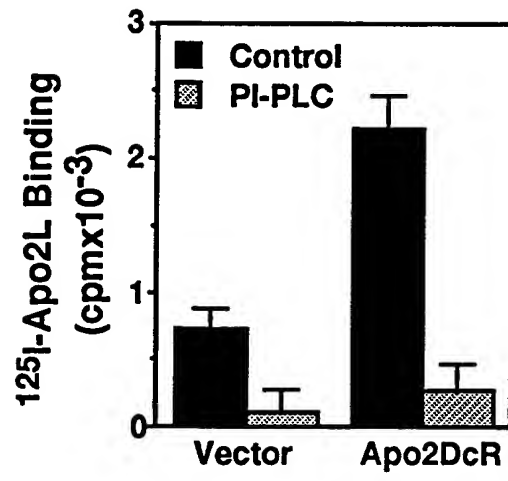


Figure 4

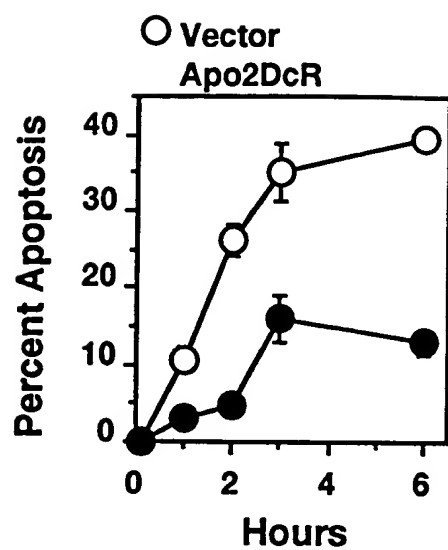


Figure 5

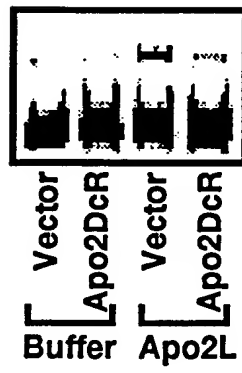


Figure 6

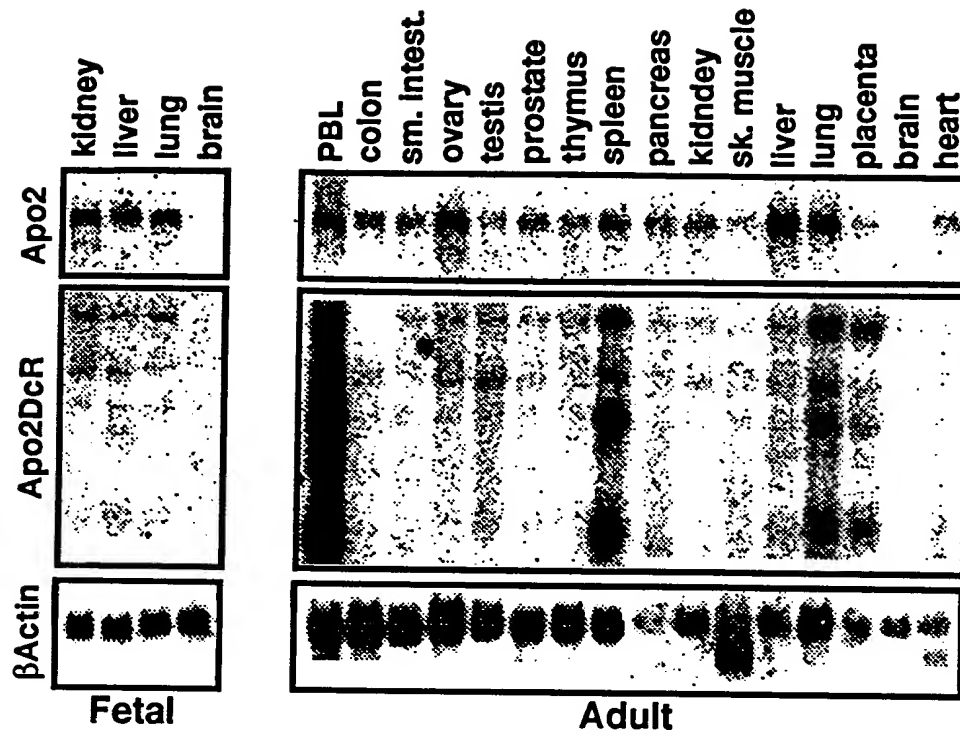


Figure 7

1	CCACGCGTC	GCATAAATC	AGCAGCGGC	CGGAGAACCC	CGCAATCTCT	GGCCCCACA	AATACACGA	CGATGCCCGA	TCTACTTTAA	GGGCTGAAAC
	GGGTGGCAG	CGGTATTAG	TCGTGGCGC	GCCTCTTGG	CGTTAGAGA	CGCGGTGTT	TTATGTGGCT	GCTACGGGCT	AGATGAAAT	CCGACTTTG
101	CCACGGCCT	GAGAGACTAT	AAGAGCGTTC	CCTACCGCCA	TGGAACAAC	GGACAGAAG	GGCCCCGGC	CTTCGGGGC	CCGAAAAGG	CACGGCCAG
1	GGTCCCGGA	CTCTCTGATA	TTCTCGCAAG	GGATGGCGGT	ACCTGTGTC	CCCTGTCTG	CGGGCCCGC	GAAGCCCGC	GGCCTTTTC	GTCCGGGTC
				M	etGluGln	gGlyGln	AlaProAla	laserGly	aArgLys	HisGlyProGly
201	GACCCAGGA	GGCGCGGGA	GCCAGGCCTG	GGTCCGGGT	CCCCAAGACC	CTTGTGCTCG	TTGTCCCGC	GGTCTGCTG	TTGGTCTCAG	CTGAGTCTGC
22	CTGGTCCCT	CCGCGCCCT	CGGTCCGGAC	CCGAGGCCA	GGGTCTCTG	GAACACGAG	AACAGCGCG	CCAGGACGAC	AACAGAGTC	GACTCAGACG
	ProArgGly	uAlaArgGly	AlaArgProG	lyLeuArgva	lProLysThr	LeuValLeu	alValAla	avalLeu	LeuValser	laGluSerAla
301	TCTGATCAC	CAACAAGACC	TAGTCCCCA	GCAGAGAGC	GGCCCCAAC	AAAAGAGGC	CAGCCCCCA	GAGGATGAT	GTCCACCTGG	ACACCATATC
	AGACTAGTG	GTGTTCTTG	ATCGAGGGT	CGTCTCTCG	CGGGGTGTC	TTTTCTCCAG	GTCCGGGAGT	CTCCCTAAC	CAGGTGGACC	TGTGGTATAG
55	LeuileThr	GlnGlnAspL	euAlaProG	nGlnArgAla	AlaProGln	InLysArgse	rSerProser	GluclyLeu	ysProProG	yHisHisile
401	TCAGAAGAC	GTAGAGATTG	CATCTCCTG	AAATATGGC	AGGACTATAG	CACCTACTGG	AATGACCTCC	TTTTCTGCTT	CGGCTGCACC	AGGTGTGATT
88	serGluAspG	lyArgAspCy	sileSerCys	LystyrGly	InAspTyrse	rThrHisTrp	AsnAspLeu	eupheCysLe	uArgCysThr	ArgCysAspser
501	CAGGTGAAGT	GGAGCTAAGT	CCCTGCACCA	CGACCAAGAA	CACAGTGTGT	CAGTGGGAA	AAGGCACCTT	CCGGGAAGAA	GATTCTCCTG	AGATGTGCCG
122	GlyGluva	lGluLeuser	ProCysThrt	hrThrArgas	nThrValcys	GlnCysGlu	luclyThrPh	eArgGluGlu	AspserProG	lucMetCysArg
601	GAAGTCCGC	ACAGGGTGT	CCAGAGGGAT	GGTCAAGGT	GGTATTGTA	CACCTGGAG	TGACATCGAA	TGTGTCCACA	AAGAATCAGG	CATCATCATATA
	CTTACCGGC	TGTCACACAG	GGTCTCCCTA	CCAGTTCCAG	CCACTAACAT	GTGGGACCTC	ACTGTAGCTT	ACACAGGTGT	TTCTTAGTCC	GATAGTAGTAT
155	LysCysArg	ThrGlyCysP	roArgGlyMe	tValLysVal	GlyAspCysT	hrProTrpse	rAspIleGlu	CysValHisL	ysGluSerG	ylelleille
701	GGAGTCACAG	TTGACGCCGT	AGTCTTGATT	GTGGCTGTGT	TTGTTTGCA	GTCTTTACTG	TGGAAGAAAG	TCCTTCCTTA	CCTGAAAGGC	ATCTGCTCAG
	CCTCAGTGT	AACGTGGCA	TCAGAACTAA	CACCGACACA	AACAAACGTT	CAGAAATGAC	ACCTTCTTTC	AGGAAGGAAT	GGACTTTCCG	TAGACGAGTC
188	GlyValThr	alAlaAlaVa	lValleuile	ValAlaValP	heValCysLy	sSerLeuLeu	TrpLysLysv	alleuProTy	rLeuLysGly	ileCysSerGly
801	GTGGTGGTG	GGACCTTGAG	CGTGTGGACA	GAAGCTCACA	ACGACCTGGG	GCTGAGGACA	ATGTCTCTCA	TGAGATCGTG	AGTATCTTGC	AGCCCCACCA
	CACCAACACC	CCTGGGACTC	GCACACCTGT	CTTCGAGTGT	TGCTGGACCC	CGACTCCTGT	TACAGGAGTT	ACTCTAGCAC	TCATAGAACC	TCGGGTGGGT
222	GlyGlyG	YaspProGlu	ArgValAspA	rgSerSerG	nArgProGly	AlaGluAspA	snValleuAs	nGluilleVal	serilleLeu	lnProThrGln
901	GGTCCCTGAG	CAGGAAATGG	AAGTCCAGGA	GCCAGCAGAG	CCAACAGGTG	TCAACATGTT	GTCCCCCGGG	GAGTCAGAGC	ATCTGCTGGA	ACCGGCAGAA
	CCAGGGACTC	GTCTTTTACC	TTCAGGTCTC	CGGTCTCTC	GGTGTCTCC	AGTTGTACAA	CAGGGGGCCC	CTCAGTCTCG	TAGACGACCT	TGGCCGTCTT
255	ValProGlu	GlnGluMetG	luValGlnG	uProAlaGlu	ProThrGlyv	alAsnMetLe	uSerProGly	GluserGluH	isLeuLeuG	uProAlaGlu
1001	GCTGAAAGGT	CTCAGAGGAG	GAGGCTGCTG	GTCCAGCAA	ATGAAGGTGA	TCCCACCTGAG	ACTCTGAGAC	GAGTCAGAGC	ATCTGCTGGA	ACCGGCAGAA
	CGACTTTCCA	GAGTCTCTC	CTCCGACGAC	CAAGGTCTGT	TACTTCCACT	AGGTGACTC	TGAGACTCTG	TCACGAAGCT	ACTGAAACGT	CTGAACCCAG
288	AlaGluArg	erglnArgar	gargLeuLeu	valProAla	snGluGlyAs	pProThrGlu	ThrLeuArg	lnCysPheAs	paspPheAla	AspLeuValPro

1101 CCTTTGACTC CTGGGAGCCG CTCATGAGGA AGTTGGGCTT CATGGAAORATTTTGGGCTAAAAGC TGAGGCAGCG GCCACACAGG ACACCTTGTA
GGAACCTGAG GACCCCTCGC GAGTACTCCT TCAACCCGGA GTACCTGTTA CTCTATTTCG ACCGATTTCG ACTCCGTGCG CCGGTGTCCC TGTGGAACAT
322 PheAspSe rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluileLysV alalalysAl aGlualaAla GlyHisArgA spThrLeuTyr
1201 CACGATGCTG ATAAAGTGGG TCAACAAAAC CGGGCGAGAT GCCTCTGTCC ACACCCTGCT GGATGCCTTG GAGACGCTGG GAGAGAGACT TGCCAAGCAG
GTGCTACGAC TATTTACACC GTTGTCTTGG GCGGCTCTA CCGAGACAGG TGTGGGACGA CCTACGGAAC CTCTGGGACC CTCTCTCTGA ACGGTTCTC
355 ThrMetLeu IleLysTrpV alasnLysTh rGlyArgAsp AlaservAlH isThrLeule uaspAlaleu GluThrLeug lyGluArgle ualalysGln
1301 AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGTTTCATGT ATCTAGAAGG TAATGCAGAC TCTGCCWGTG CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA
TTCTAACTCC TGGTGAACAA CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGTCTG AGACGGAACA GGATTACAC GATTACACTCT
388 LysIleGluA spHisLeuLe uSerSerGly LysPheMetT yrLeuGluGl yAsnAlaasp SerAlaXqqS erOC*
1401 CCTTCCCTGG TTTACCTTTT TTCTGGAAA AGCCCAACTG GACTCCAGTC AGTAGGAAAAG TGCCACAATT GTCACATGAC CCGTACTGGA AGAAACTCTC
GGAAGGGACC AAATGGAAA AAGACCTTTT TCGGGTTGAC CTGAGGTCAG TCATCCTTTC ACGGTGTTAA CAGTGTACTG GCCATGACCT TCTTTGAGAG
1501 CCATCCAAAC TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAT
GGTAGGTTGT AGTGGGTCAC CTACCTTGTA GGACATTGAA AAGTGACGTG AACCGTAATA AAAATATTTCG ACTTACACTA TTATTCTCTGT GATACCTTTA
1601 GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTTT TGGGATGTCA TTGTTTTTCAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT
CAGACCTAGT AAGGCAAAACA CGCATGAAAC TCTAAACCAA ACCCTACAGT AACAAAAGTG TCGTGAAAAA ATAGGATTAC ATTTACGAAA TAAATAAATA
1701 TTGGGGTACA TTGTAAGATC CATCTACAAA AAAAAAAAAG GCGGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC
AACCCGATGT AACATTCTAG GTAGATGTTT TTTTTTTTTT CCGCCGGCGC TGAGATCTCA GCTGGACGTC TTCGAACCCG CCGTACCCG

Fig. 8 (cont.)

Fig. 9

1 MEORGONAPAAAGARKRHGPGPREARGARPGRLRVPKTLVLVVAALLLVSAESALITQQD
61 LAFQRAAPQOKRSSPSEGLCPPGHHISEDGRDCISCKYQDYSTHWNDLLFCLRCTRCD
121 SGEVELSPCTTTRNTVCQCEEGTFREEDSPERMCRKCRKGPRGMVKVGDCTPWSDDIECVH
181 KESGIIIGVTVAAVLIVAVFCKSLLKKVLPYLKICSGGGGDPERVDRSSQRRPGEAD
241 NVLNEIVSILQPTQVPEQEMEVOEPAEPTGVNMLSPGESEHLLLEPAEERSQRRRLVPA
301 NEGDPTELRQCFDDFADLVPFDSWEPLMRKLGIMDNEIKVAKAEAAAGHRDTLYTMLIKW
361 VNKTGRDASVHTLLDALETGLGERLAKQKIEDHLLSSGKFMYLEGNADSAIS

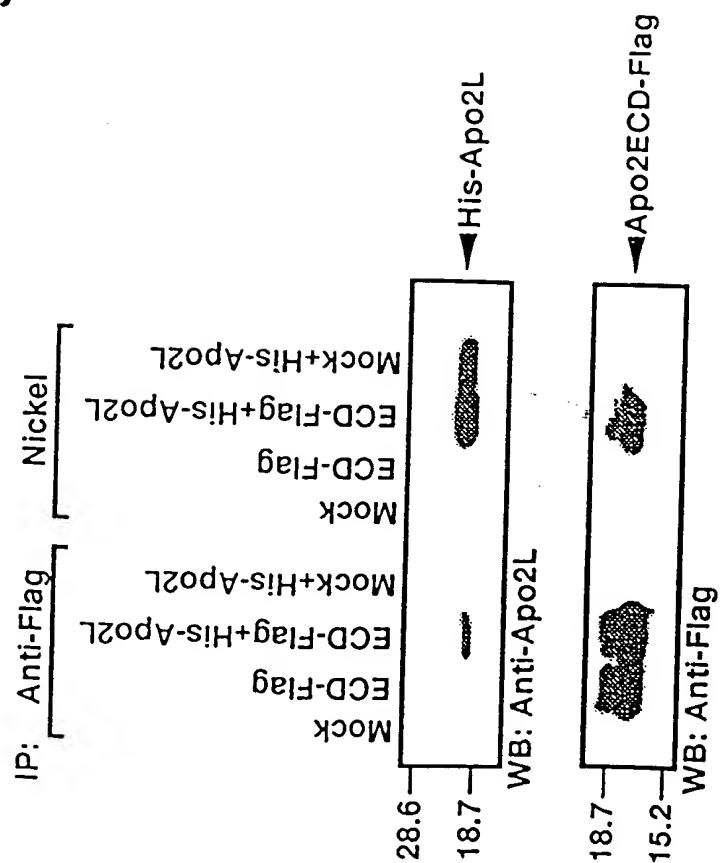
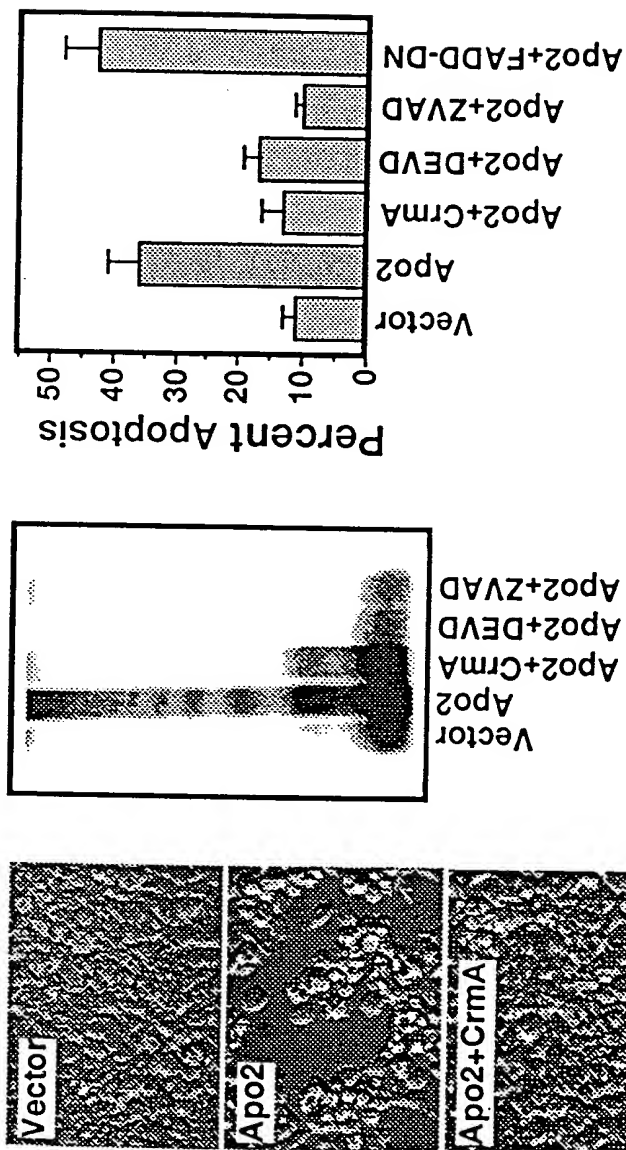
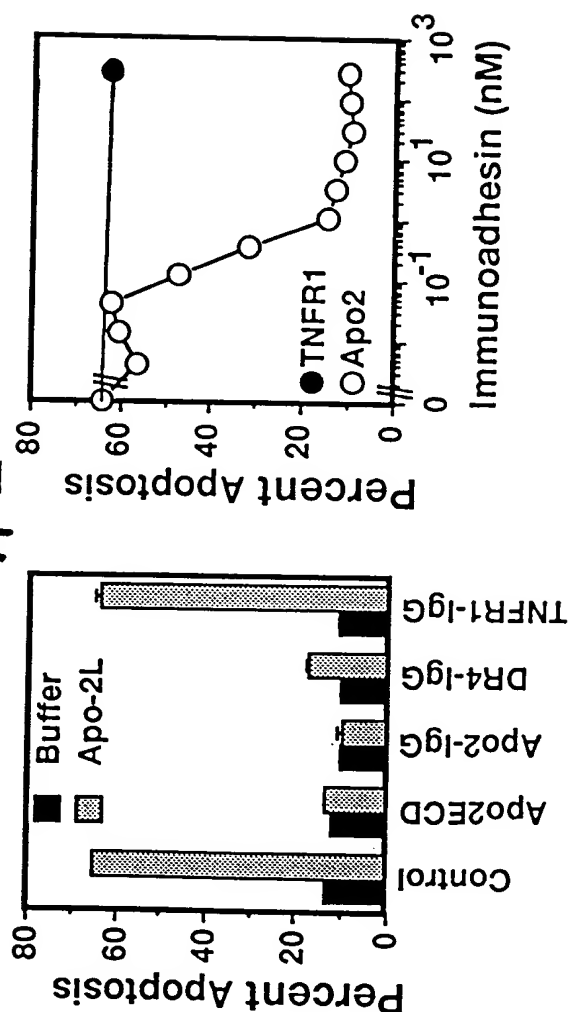


Fig. 11

11 A 11 B 11 C



11 D 11 E



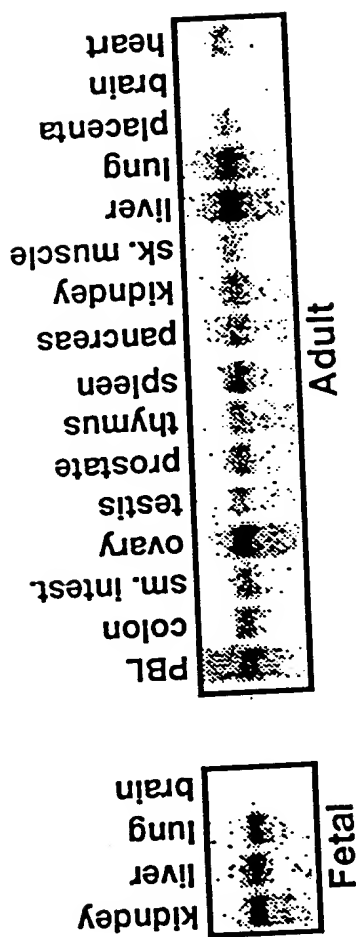


FIG. 13